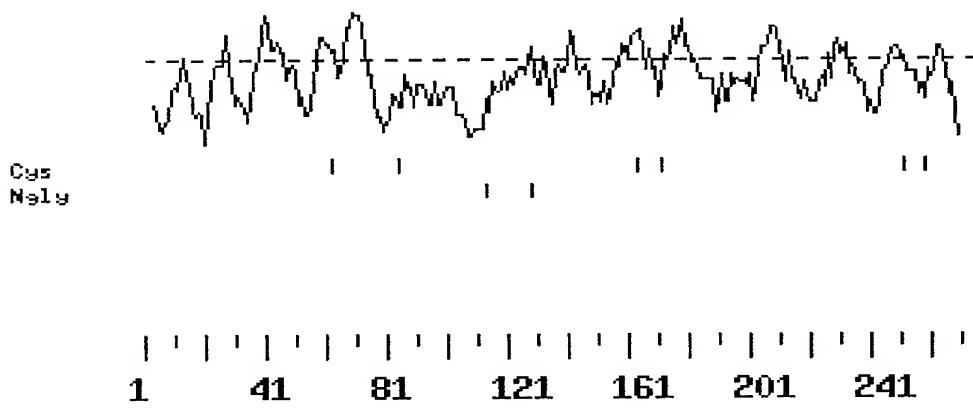


**Figure 1**

**adh\_short: domain 1/1, from 37 to 249: score 135.6, E=9.1e-37**

Begin SEQ ID NO:7	* ->	KvalVLTGassGIGlaiAkrLakeGakVvvadrneeklekg . . . . .
	+v+L+TGA+SG+G+	A++a++ a +v+ d+n e+ + ++
SEQ ID NO:2 (21617)	37	QVCLITGAGSGLGRLFALFARRRALLVLWDINTQSNEETagmvrhi 83
		.....avakelkelGgnd . . . . . kdrAlaiq1Dvtdeesvkaaveqav
	++ +ac+ +++ ++G++ ++	++ +e+ +r++ DV ++e V ++e++
21617	84	yrdleAADAAALQAGNGEEeilphcNLQVFITYTCDVVGKRENVYLTAAERV 133
		er1GrG1DvLVNNAGGi1llrpgpfaelsrtmeedwdrvividvN1tgvf11
	+++G + vLVNNAG	+ +e + +e++r++ VN ++ f++
21617	134	KEVGE-VSVLVNNAG--V-VSGHHLLECP---DELIERTMVNCHAHFWT 176
		travlp1mamkkrqgGrIVNiSSVaGrkegg1vgvpqgsaysASKaAvig
	t+a+1p m++ +G IV++S G 1	+g Y+ASK++v+g
21617	177	TKAFLP--TMLIEINHGHIVTVASSLG----LFSTAGVEDYCASKFGVVG 219
		1trsLAE1aphg . . gIrvnavaPGgvdTd <- * End SEQ ID NO:7
	+ +SL +E1 + +GI +	V+P vdT
21617	220	FHESSLSELKAAEkdGIKTTLVCPTYLVDTG 249 SEQ ID NO:2

**Figure 2**



**Figure 3**

**TPR: domain 1 of 1, from 40 to 73: score 7.5, E = 7.2**

Begin SEQ ID NO:8 \*-> aeayyn1Gnay1klgkydeAiedyekALeldPnn <-\* End SEQ ID NO:8  
a + +++ + +Y +A+ +Y++ ++L +  
SEQ ID NO:5 (55562) 40 AATVLKRAVELDSESRYPQALVVCYQEGIDLLLQV 73

**Figure 4**

**PD314595 p2001.1 (1)**

Score = 386 (140.9 bits), Expect = 6.8e-36, P = 6.8e-36  
 Identities = 80/228 (35%), Positives = 126/228 (55%)

Begin SEQ ID NO: 9 \*-> AKELLIRAVECDQVNGRILEAQQTLYTTEGIGQLMQFVNNGEPDEAKRKGFILTTRIKEYMDRA  
 A +L RAVE D R +A Y EGI L+Q + G D KR +I +YMDRA+  
 SEQ ID NO: 5 (55562) 40 AATVLKRAVELDSESRYPQALVVCYQEGIDLLLQVLKGTKDNTKRCNLREREKISKYMDRAEN 99

IKARINGKLMILGEVVSHVSIDENDTGFDYDQLEFGKYMDDKTVEIMLEEPYMTQNYQQYQNL  
 IK ++ + G+ + I+EN TGF Y+ LF +Y++ E+ +E+PY+ +Q N  
 55562 100 IKKYLDQEKGKYHKQIKIEENATGFSYESSLFREYLNETVTVEWVIEDPYIRHTHQLYNF 159

IRFLELAATNCPNLKYFRLLITKEYDAKNPDQEQETNLGQIKGDLERRRNVTVVYIKYEDSLH  
 +RF E+ +K L+T + QQ L +I+ L V + +Y S+H  
 55562 160 LRFCEMLIKRPCVKVTKIHLITS-LDEGIEQVQQSRGLQEIEESLRSHGVILLEVQYSSSIH 218

DRKIYLSNGYIIKIGRGLHFYKPANPMYSIGLVNYKFRKCLQTVDIW <- \* End SEQ ID NO: 9  
 DR+I +NG+IKIGRGL +K +S+G ++ R C +T VDI+  
 55562 219 DREIRFNNGWMIKIGRGLDYFKKPKQSRSFLGYCDFDLRPCHETTVDIF 266 SEQ ID NO: 2

**Figure 5**

**PD014461 p99.2 (4)**

Score = 84 (34.6 bits), Expect = 0.0019, P = 0.0019  
Identities = 18/59 (30%), Positives = 32/59 (54%)

Begin SEQ ID NO:10 \*-> AIDLVQKAIDEDKAGQYEEAYQLYQHALDYFMHALKYEAKNDKSKEIIRAKC  
A +++A++ D +Y +A YQ +D + LK N K + R K  
SEQ ID NO:5 (55562) 40 AATVILKRAVELDSESSRYPQALVCYQEGFIDLLQVILKGTKDNTKRCNLI-REKI 90

TEYLDR <-\* End SEQ ID NO:10  
++Y+DRA  
55562 91 SKYMDRA 97 SEQ ID NO:5

**Figure 6**